

RECEIVED

MAR 1 10 21 13

TECH CENTER 1000/2000

1600

RAW SEQUENCE LISTING

DATE: 03/04/2003

PATENT APPLICATION: US/09/105,117K

TIME: 15:37:48

Input Set : A:\Seq_listing_US_korrigiert130203.txt

Output Set: N:\CRF4\03042003\I105117K.raw

3 <110> APPLICANT: Forschungszentrum Juelich GmbH; Marina Vrlijc et al.
 5 <120> TITLE OF INVENTION: Process for the microbial production of amino acids by
 6 boosted activity of export carriers
 8 <130> FILE REFERENCE: 1
 10 <140> CURRENT APPLICATION NUMBER: US/09/105,117K
 11 <141> CURRENT FILING DATE: 1998-06-17
 12 <150> PRIOR APPLICATION NUMBER: PCT/DE96/02485
 13 <151> PRIOR FILING DATE: 1996-12-18
 W--> 14 <160> NUMBER OF SEQ ID: 5
 16 <170> SOFTWARE: PatentIn Ver. 2.0
 18 <210> SEQ ID NO: 1
 19 <211> LENGTH: 2374
 20 <212> TYPE: DNA
 21 <213> ORGANISM: Corynebacterium glutamicum
 W--> 22 <220> FEATURE:
 23 <221> NAME/KEY: gene
 24 <222> LOCATION: CDS (1016)..(1726)
 25 <223> OTHER INFORMATION: (Lyse)
 27 <400> SEQUENCE: 1
 28 ccatttgctg aaggtgttac tctgcctggc ccaattcctg cgggcgaaga agtgaaaaac 60
 30 cctgaacctt ttcagaagta actaaggccg caatccctcg attgctgcat caacgacggc 120
 32 gtctgtgagt ctagctagag atctagattc caggcgccat cgttgccaat acatcgggtg 180
 34 gtcaatgggt atctcatcga ggaggatcac ttctcctgct tttagcatgg gagcagcttg 240
 36 ggtttcggga agaagtcgcc aaccaaggcc tcggcgcaatt gcctcaccaa aaccttcgcg 300
 38 cgacgggaca atggatacgc gcctgcgccc cacaggacca tcgacgcgcc cgtccaggtc 360
 40 acggtcttga agcacatctt tgggaccgaa gcgtaagacg ggcacgcgag cccaatctag 420
 42 ttcccatca accatgtagg catcccgcaa tgagggggtt gcaatggcca agtggcgcat 480
 44 ggttccaagt tctactactt cacatccgcg cacgggatta gcttcacggg ttaccgctcc 540
 46 taaaacatct ccacgcgcga gcaaggataa tgtgtgcgct tcatcttcca agcgcagcgt 600
 48 gagcgttgct ccaccccaag aagctacctc gttgaacacg ggaggaaacc atgtggatag 660
 50 cgaatctgcg ttgatggcga tggttaacgg gatttcagca aggcgtccag atagtgcgcg 720
 52 tttagtttct gcttgacgca acaccatttt ccgcgctgct tgcacaagga cttcacccgc 780
 54 ttoggttgct ttggccgggt gggtgcgcga taccaacact cgaccacgt gatgctcgag 840
 56 agctttaacg cgctgactca ccgcccaggg ggaatggaa agggctaagg aggcgccttc 900
 59 gaagctgcct tcatcaatga ttgagagcaa agtgtccagt tgaatgggt tcatgaagct 960
 61 atattaaacc atgttaagaa ccaatcattt tacttaagta cttccatagg tcacg atg 1018
 62 Met
 63 1
 65 gtg atc atg gaa atc ttc att aca ggt ctg ctt ttg ggg gcc agt ctt 1066
 66 Val Ile Met Glu Ile Phe Ile Thr Gly Leu Leu Leu Gly Ala Ser Leu
 67 5 10 15
 69 tta ctg tcc atc gga ccg cag aat gta ctg gtg att aaa caa gga att 1114
 70 Leu Leu Ser Ile Gly Pro Gln Asn Val Leu Val Ile Lys Gln Gly Ile

ENTERED

RAW SEQUENCE LISTING

DATE: 03/04/2003

PATENT APPLICATION: US/09/105,117K

TIME: 15:37:48

Input Set : A:\Seq_listing_US_korrigiert130203.txt

Output Set: N:\CRF4\03042003\I105117K.raw

```

71          20          25          30
73 aag cgc gaa gga ctc att gcg gtt ctt ctc gtg tgt tta att tct gac 1162
74 Lys Arg Glu Gly Leu Ile Ala Val Leu Leu Val Cys Leu Ile Ser Asp
75          35          40          45
77 gtc ttt ttg ttc atc gcc ggc acc ttg ggc gtt gat ctt ttg tcc aat 1210
78 Val Phe Leu Phe Ile Ala Gly Thr Leu Gly Val Asp Leu Leu Ser Asn
79 50          55          60          65
81 gcc gcg ccg atc gtg ctc gat att atg cgc tgg ggt ggc atc gct tac 1258
82 Ala Ala Pro Ile Val Leu Asp Ile Met Arg Trp Gly Gly Ile Ala Tyr
83          70          75          80
85 ctg tta tgg ttt gcc gtc atg gca gcg aaa gac gcc atg aca aac aag 1306
86 Leu Leu Trp Phe Ala Val Met Ala Ala Lys Asp Ala Met Thr Asn Lys
87          85          90          95
89 gtg gaa gcg cca cag atc att gaa gaa aca gaa cca acc gtg ccc gat 1354
90 Val Glu Ala Pro Gln Ile Ile Glu Glu Thr Glu Pro Thr Val Pro Asp
91          100          105          110
93 gac acg cct ttg ggc ggt tcg gcg gtg gcc act gac acg cgc aac cgg 1402
94 Asp Thr Pro Leu Gly Gly Ser Ala Val Ala Thr Asp Thr Arg Asn Arg
95          115          120          125
97 gtg cgg gtg gag gtg agc gtc gat aag cag cgg gtt tgg gta aag ccc 1450
98 Val Arg Val Glu Val Ser Val Asp Lys Gln Arg Val Trp Val Lys Pro
99 130          135          140          145
101 atg ttg atg gca atc gtg ctg acc tgg ttg aac ccg aat gcg tat ttg 1498
102 Met Leu Met Ala Ile Val Leu Thr Trp Leu Asn Pro Asn Ala Tyr Leu
103          150          155          160
105 gac gcg ttt gtg ttt atc gcc ggc gtc gcc gcg caa tac gcc gac acc 1546
106 Asp Ala Phe Val Phe Ile Gly Gly Val Gly Ala Gln Tyr Gly Asp Thr
107          165          170          175
109 gga cgg tgg att ttc gcc gct gcc gcg ttc gcg gca agc ctg atc tgg 1594
110 Gly Arg Trp Ile Phe Ala Ala Gly Ala Phe Ala Ala Ser Leu Ile Trp
111          180          185          190
113 ttc ccg ctg gtg ggt ttc gcc gca gca gca ttg tca cgc ccg ctg tcc 1642
114 Phe Pro Leu Val Gly Phe Gly Ala Ala Ala Leu Ser Arg Pro Leu Ser
115          195          200          205
117 agc ccc aag gtg tgg cgc tgg atc aac gtc gtc gtg gca gtt gtg atg 1690
118 Ser Pro Lys Val Trp Arg Trp Ile Asn Val Val Val Ala Val Val Met
119 210          215          220          225
121 acc gca ttg gcc atc aaa ctg atg ttg atg ggt tag ttttcgcggg 1736
122 Thr Ala Leu Ala Ile Lys Leu Met Leu Met Gly
123          230          235
125 ttttggaatc ggtggccttc gcccaaagt tgaatcggc gtcgtgggaa atctcatcga 1796
127 tcgcctccaa ctgcgcgtca gaaaactcca agttgttgag tgaatcaagg ctgttggtcca 1856
129 gctgctcaac tgacgaagca ccaatcaatg cactggtcac ggtatccgcg ccgtactctc 1916
131 cttgctcgcg cagcaccat gcaagcgcca tctgcgcaag tgactgcccg cgttcctggg 1976
133 cgatgtcatt gagcttgccg accatatcaa tattgttcac gttcaacatg cctcagaca 2036
135 gggacttacc ctggctggcg cggaaccct ctggaattcc atcgagatat ttgtccgtga 2096
137 gcaggccctg cgcaagtgt gagaaagcaa tgacgccaa accattgttg gcagctgact 2156
139 gcaacaagtt ctaccgtca tcgccggtt cctccacca acgattaatg atggaatagc 2216
141 ttggctgatg aatcagaagc gggcagccct cctccgcat gaactcagcc gcctccgctg 2276

```

RAW SEQUENCE LISTING

DATE: 03/04/2003

PATENT APPLICATION: US/09/105,117K

TIME: 15:37:48

Input Set : A:\Seq_listing_US_korrigiert130203.txt

Output Set: N:\CRF4\03042003\I105117K.raw

```

143 tgagctctgg accgtaggaa gaaataccca cgtaaagagc ctttccagac gcaacaatgt 2336
145 cacgcaatgc gtacatggtt tcttccaaag gagtatct 2374
150 <210> SEQ ID NO: 2
151 <211> LENGTH: 236
152 <212> TYPE: PRT
153 <213> ORGANISM: Corynebacterium glutamicum
W--> 154 <220> FEATURE:
155 <223> OTHER INFORMATION: (LysE)
157 <400> SEQUENCE: 2
158 Met Val Ile Met Glu Ile Phe Ile Thr Gly Leu Leu Leu Gly Ala Ser
159 1 5 10 15
161 Leu Leu Leu Ser Ile Gly Pro Gln Asn Val Leu Val Ile Lys Gln Gly
162 20 25 30
164 Ile Lys Arg Glu Gly Leu Ile Ala Val Leu Leu Val Cys Leu Ile Ser
165 35 40 45
167 Asp Val Phe Leu Phe Ile Ala Gly Thr Leu Gly Val Asp Leu Leu Ser
168 50 55 60
170 Asn Ala Ala Pro Ile Val Leu Asp Ile Met Arg Trp Gly Gly Ile Ala
171 65 70 75 80
173 Tyr Leu Leu Trp Phe Ala Val Met Ala Ala Lys Asp Ala Met Thr Asn
174 85 90 95
176 Lys Val Glu Ala Pro Gln Ile Ile Glu Thr Glu Pro Thr Val Pro
177 100 105 110
179 Asp Asp Thr Pro Leu Gly Gly Ser Ala Val Ala Thr Asp Thr Arg Asn
180 115 120 125
182 Arg Val Arg Val Glu Val Ser Val Asp Lys Gln Arg Val Trp Val Lys
183 130 135 140
185 Pro Met Leu Met Ala Ile Val Leu Thr Trp Leu Asn Pro Asn Ala Tyr
186 145 150 155 160
188 Leu Asp Ala Phe Val Phe Ile Gly Gly Val Gly Ala Gln Tyr Gly Asp
189 165 170 175
191 Thr Gly Arg Trp Ile Phe Ala Ala Gly Ala Phe Ala Ala Ser Leu Ile
192 180 185 190
194 Trp Phe Pro Leu Val Gly Phe Gly Ala Ala Ala Leu Ser Arg Pro Leu
195 195 200 205
197 Ser Ser Pro Lys Val Trp Arg Trp Ile Asn Val Val Val Ala Val Val
198 210 215 220
200 Met Thr Ala Leu Ala Ile Lys Leu Met Leu Met Gly
201 225 230 235
207 <210> SEQ ID NO: 3
208 <211> LENGTH: 2374
209 <212> TYPE: DNA
210 <213> ORGANISM: Corynebacterium glutamicum
W--> 211 <220> FEATURE:
212 <221> NAME/KEY: unsure
213 <222> LOCATION: CDS (2)..(652)
214 <223> OTHER INFORMATION: orf3
215 (complement to SEQ ID No. 1)
W--> 216 <220> FEATURE:

```

RAW SEQUENCE LISTING

DATE: 03/04/2003

PATENT APPLICATION: US/09/105,117K

TIME: 15:37:48

Input Set : A:\Seq_listing_US_korrigiert130203.txt

Output Set: N:\CRF4\03042003\I105117K.raw

```

217 <221> NAME/KEY: gene
218 <222> LOCATION: CDS (1421)..(2293)
219 <223> OTHER INFORMATION: LysG
221 <400> SEQUENCE: 3
222 a gat act cct ttg gaa gaa acc atg tac gca ttg cgt gac att gtt gcg 49
223   Asp Thr Pro Leu Glu Glu Thr Met Tyr Ala Leu Arg Asp Ile Val Ala
224     1           5           10           15
226 tct gga aag gct ctt tac gtg ggt att tct tcc tac ggt cca gag ctc 97
227 Ser Gly Lys Ala Leu Tyr Val Gly Ile Ser Ser Tyr Gly Pro Glu Leu
228           20           25           30
230 aca gcg gag gcg gct gag ttc atg gcg gag gag ggc tgc ccg ctt ctg 145
231 Thr Ala Glu Ala Ala Glu Phe Met Ala Glu Glu Gly Cys Pro Leu Leu
232           35           40           45
234 att cat cag cca agc tat tcc atc att aat cgt tgg gtg gag gaa ccg 193
235 Ile His Gln Pro Ser Tyr Ser Ile Ile Asn Arg Trp Val Glu Glu Pro
236     50           55           60
238 ggc gat gac ggt gag aac ttg ttg cag tca gct gcc aac aat ggt ctt 241
239 Gly Asp Asp Gly Glu Asn Leu Leu Gln Ser Ala Ala Asn Asn Gly Leu
240   65           70           75           80
242 ggc gtc att gct ttc tca cca ctt gcg cag ggc ctg ctc acg gac aaa 289
243 Gly Val Ile Ala Phe Ser Pro Leu Ala Gln Gly Leu Leu Thr Asp Lys
244           85           90           95
246 tat ctc gat gga att cca gag ggt tcc cgc gcc agc cag ggt aag tcc 337
247 Tyr Leu Asp Gly Ile Pro Glu Gly Ser Arg Ala Ser Gln Gly Lys Ser
248           100          105          110
250 ctg tct gag ggc atg ttg aac gtg aac aat att gat atg gtc cgc aag 385
251 Leu Ser Glu Gly Met Leu Asn Val Asn Asn Ile Asp Met Val Arg Lys
252           115          120          125
254 ctc aat gac atc gcc cag gaa cgc ggg cag tca ctt gcg cag atg gcg 433
255 Leu Asn Asp Ile Ala Gln Glu Arg Gly Gln Ser Leu Ala Gln Met Ala
256           130          135          140
258 ctt gca tgg gtg ctg cgc gag caa gga gag tac ggc gcg gat acc gtg 481
259 Leu Ala Trp Val Leu Arg Glu Gln Gly Glu Tyr Gly Ala Asp Thr Val
260 145           150          155          160
262 acc agt gca ttg att ggt gct tcg tca gtt gag cag ctg gac aac agc 529
263 Thr Ser Ala Leu Ile Gly Ala Ser Ser Val Glu Gln Leu Asp Asn Ser
264           165          170          175
266 ctt gat tca ctc aac aac ttg gag ttt tct gac gcc gag ttg gag gcg 577
267 Leu Asp Ser Leu Asn Asn Leu Glu Phe Ser Asp Ala Glu Leu Glu Ala
268           180          185          190
270 atc gat gag att tcc cac gac gcc ggc atc aac att tgg gcg aag gcc 625
271 Ile Asp Glu Ile Ser His Asp Ala Gly Ile Asn Ile Trp Ala Lys Ala
272           195          200          205
274 acc gat tcc aaa acc cgc gaa aac taa cccatcaaca tcagtttgat 672
275 Thr Asp Ser Lys Thr Arg Glu Asn
276   210          215
278 ggccaatgcg gtcacacaaa ctgccacgac gacgttgatc cagcgccaca ccttggggct 732
280 ggacagcggg cgtgacaatg ctgctgcgcc gaaaccacac agcggaacc agatcaggct 792
282 tgccgcgaac gcgccagcgg cgaaaatcca ccgtccggtg tcgccgtatt gcgcgccgac 852

```

RAW SEQUENCE LISTING

DATE: 03/04/2003

PATENT APPLICATION: US/09/105,117K

TIME: 15:37:48

Input Set : A:\Seq_listing_US_korrigiert130203.txt

Output Set: N:\CRF4\03042003\I105117K.raw

```

284 gccgccgata aacacaaacg cgtccaaata cgcattcggg ttcaaccagg tcagcacgat 912
286 tgccatcaac atgggcttta cccaaaccg ctgcttatcg acgctcacct ccaccgcac 972
288 ccggttgccg gtgtcagtg ccaccgccga accgcccaaa ggcgtgtcat cgggcacggg 1032
290 tggttctggt tcttcaatga tctgtggcgc ttccaccttg tttgtcatgg cgtctttcgc 1092
292 tgccatgacg gcaaaccata acaggtaac gatgccacc cagcgcataa tatcgagcac 1152
294 gatcggcgcg gcattggaca aaagatcaac gcccaagggt cgcgcgatga acaaaaagac 1212
296 gtcagaaatt aaacacacga gaagaaccgc aatgagtcct tcgcgcttaa ttccttggtt 1272
298 aatcaccagt acattctgcg gtccgatgga cagtaaaaga ctggccccc aaagcagacc 1332
300 tgtaatgaag atttccatga tcaccatcgt gacctatgga agtacttaag taaaatgatt 1392
302 ggttcttaac atggtttaat atagcttc atg aac ccc att caa ctg gac act 1444
303 Met Asn Pro Ile Gln Leu Asp Thr
W--> 304 220 225
306 ttg ctc tca atc att gat gaa ggc agc ttc gaa ggc gcc tcc tta gcc 1492
307 Leu Leu Ser Ile Ile Asp Glu Gly Ser Phe Glu Gly Ala Ser Leu Ala
W--> 308 230 235 240
310 ctt tcc att tcc ccc tcg gcg gtg agt cag cgc gtt aaa gct ctc gag 1540
311 Leu Ser Ile Ser Pro Ser Ala Val Ser Gln Arg Val Lys Ala Leu Glu
W--> 312 245 250 255
314 cat cac gtg ggt cga gtg ttg gta tcg cgc acc caa ccg gcc aaa gca 1588
315 His His Val Gly Arg Val Leu Val Ser Arg Thr Gln Pro Ala Lys Ala
W--> 316 260 265 270
318 acc gaa gcg ggt gaa gtc ctt gtg caa gca gcg cgg aaa atg gtg ttg 1636
319 Thr Glu Ala Gly Glu Val Leu Val Gln Ala Ala Arg Lys Met Val Leu
W--> 320 275 280 285
322 ctg caa gca gaa act aaa gcg caa cta tct gga cgc ctt gct gaa atc 1684
323 Leu Gln Ala Glu Thr Lys Ala Gln Leu Ser Gly Arg Leu Ala Glu Ile
W--> 324 290 295 300 305
326 ccg tta acc atc gcc atc aac gca gat tcg cta tcc aca tgg ttt cct 1732
327 Pro Leu Thr Ile Ala Ile Asn Ala Asp Ser Leu Ser Thr Trp Phe Pro
W--> 328 310 315 320
330 ccc gtg ttc aac gag gta gct tct tgg ggt gga gca acg ctc acg ctg 1780
331 Pro Val Phe Asn Glu Val Ala Ser Trp Gly Gly Ala Thr Leu Thr Leu
W--> 332 325 330 335
334 cgc ttg gaa gat gaa gcg cac aca tta tcc ttg ctg cgg cgt gga gat 1828
335 Arg Leu Glu Asp Glu Ala His Thr Leu Ser Leu Leu Arg Arg Gly Asp
W--> 336 340 345 350
338 gtt tta gga gcg gta acc cgt gaa gct aat ccc gtg gcg gga tgt gaa 1876
339 Val Leu Gly Ala Val Thr Arg Glu Ala Asn Pro Val Ala Gly Cys Glu
W--> 340 355 360 365
342 gta gta gaa ctt gga acc atg cgc cac ttg gcc att gca acc ccc tca 1924
343 Val Val Glu Leu Gly Thr Met Arg His Leu Ala Ile Ala Thr Pro Ser
W--> 344 370 375 380 385
346 ttg cgg gat gcc tac atg gtt gat ggg aaa cta gat tgg gct gcg atg 1972
347 Leu Arg Asp Ala Tyr Met Val Asp Gly Lys Leu Asp Trp Ala Ala Met
W--> 348 390 395 400
350 ccc gtc tta cgc ttc ggt ccc aaa gat gtg ctt caa gac cgt gac ctg 2020
351 Pro Val Leu Arg Phe Gly Pro Lys Asp Val Leu Gln Asp Arg Asp Leu
W--> 352 405 410 415
354 gac ggg cgc gtc gat ggt cct gtg ggg cgc agg cgc gta tcc att gtc 2068

```

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 03/04/2003
PATENT APPLICATION: US/09/105,117K TIME: 15:37:49

Input Set : A:\Seq_listing_US_korrigiert130203.txt
Output Set: N:\CRF4\03042003\I105117K.raw

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 1,2,3,4,5,6,7,8,9,10,11,12,14,15,16,17,18,19,20,21,22,23,24
Seq#:1; Line(s) 25,27,28,29,30,31,32,33,34,35,36,37,38,39,40,41,42,43,44,45
Seq#:1; Line(s) 46,47,48,49,50,51,52,53,54,55,56,59,60,61,62,63,64,65,66,67
Seq#:1; Line(s) 68,69,70,71,72,73,74,75,76,77,78,79,80,81,82,83,84,85,86,87
Seq#:1; Line(s) 88,89,90,91,92,93,94,95,96,97,98,99,100,101,102,103,104,105
Seq#:1; Line(s) 106,107,108,109,110,111,112,113,114,115,116,117,118,119,120
Seq#:1; Line(s) 121,122,123,124,125,126,127,128,129,130,131,132,133,134,135
Seq#:1; Line(s) 136,137,138,139,140,141,142,143,144,145,146,147,150
Seq#:2; Line(s) 151,153,157,158,159,160,161,162,163,164,165,166,167,168,169
Seq#:2; Line(s) 170,171,172,173,174,175,176,177,178,179,180,181,182,183,184
Seq#:2; Line(s) 185,186,187,188,189,190,191,192,193,194,195,196,197,198,199
Seq#:2; Line(s) 200,201,202,203,204,207
Seq#:3; Line(s) 208,209,210,211,212,213,214,215,216,222,223,224,225,226,227
Seq#:3; Line(s) 228,229,230,231,232,233,234,235,236,237,238,239,240,241,242
Seq#:3; Line(s) 243,244,245,246,247,248,249,250,251,252,253,254,255,256,257
Seq#:3; Line(s) 258,259,260,261,262,263,264,265,266,267,268,269,270,271,272
Seq#:3; Line(s) 273,274,275,276,277,278,279,280,281,282,283,284,285,286,287
Seq#:3; Line(s) 288,289,290,291,292,293,294,295,296,297,298,299,300,301,302
Seq#:3; Line(s) 303,304,305,306,307,308,309,310,311,312,313,314,315,316,317
Seq#:3; Line(s) 318,319,320,321,322,323,324,325,326,327,328,329,330,331,332
Seq#:3; Line(s) 333,334,335,336,337,338,339,340,341,342,343,344,345,346,347
Seq#:3; Line(s) 348,349,350,351,352,353,354,355,356,357,358,359,360,361,362
Seq#:3; Line(s) 363,364,365,366,367,368,369,370,371,372,373,374,375,376,377
Seq#:3; Line(s) 378,379,380,381,382,383
Seq#:4; Line(s) 384,385,386,387,389,390,391,392,393,394,395,396,397,398,399
Seq#:4; Line(s) 400,401,402,403,404,405,406,407,408,409,410,411,412,413,414
Seq#:4; Line(s) 415,416,417,418,419,420,421,422,423,424,425,426,427,428,429
Seq#:4; Line(s) 430,431,432,433,434
Seq#:5; Line(s) 435,437,438,441,442,443,444,445,446,447,448,449,450,451,452
Seq#:5; Line(s) 453,454,455,456,457,458,459,460,461,462,463,464,465,466,467
Seq#:5; Line(s) 468,469,470,471,472,473,474,475,476,477,478,479,480,481,482
Seq#:5; Line(s) 483,484,485,486,487,488,489,490,491,492,493,494,495,496,497
Seq#:5; Line(s) 498

VERIFICATION SUMMARY

DATE: 03/04/2003

PATENT APPLICATION: US/09/105,117K

TIME: 15:37:49

Input Set : A:\Seq_listing_US_korrigiert130203.txt

Output Set: N:\CRF4\03042003\I105117K.raw

L:14 M:283 W: Missing Blank Line separator, <160> field identifier
L:22 M:283 W: Missing Blank Line separator, <220> field identifier
L:154 M:283 W: Missing Blank Line separator, <220> field identifier
L:211 M:283 W: Missing Blank Line separator, <220> field identifier
L:216 M:283 W: Missing Blank Line separator, <220> field identifier
L:304 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:308 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:312 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:316 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:320 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:324 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:328 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:332 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:336 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:340 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:344 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:348 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:352 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:356 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:360 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:364 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:368 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:372 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:376 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:387 M:283 W: Missing Blank Line separator, <220> field identifier
L:438 M:283 W: Missing Blank Line separator, <220> field identifier